

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

**In re the application of:** Markus Pompejus *et al.*

**Serial No.:** Not Yet Assigned

**Filed:** Herewith

**For:** "*Corynebacterium Glutamicum Genes Encoding Metabolic Pathway Proteins*"

**Attorney Docket No.:** BGI-121CP2

**Group Art Unit:** Not Yet Assigned

**Examiner:** Not Yet Assigned

**Assistant Commissioner for Patents**

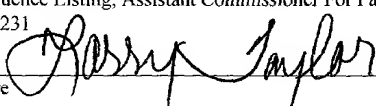
**BOX SEQUENCE LISTING**

**Washington, DC 20231**

**TRANSMITTAL LETTER FOR DISKETTE OF SEQUENCE LISTING**

Dear Sir:

Enclosed is a diskette which contains a computer readable form of the Sequence Listing for the patent application filed herewith. The Sequence Listing complies with the requirements of 37 C.F.R. §1.821. The material on this disk is identical in substance to the paper copy of the Sequence Listing appearing on pages 1 - 175, which is submitted herewith, as required by 37 CFR §1.821(f). The computer readable form of the Sequence Listing contained on the enclosed disk is understood to comply with the requirements of §1.824(d).

"Express Mail" mailing label number EL 589 739 505 US  
Date of Deposit December 22, 2000  
I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to:  
Box Sequence Listing, Assistant Commissioner For Patents, Washington, D C. 20231  
Signature   
Larry Taylor  
Please Print Name of Person Signing

LAHIVE & COCKFIELD, LLP

Attorneys at Law

By: 

Elizabeth A. Hanley  
Registration No. 33,505  
28 State Street  
Boston, MA 02109

Date: **December 22, 2000**

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## SEQUENCE LISTING

<110> Pompejus, Markus  
 Kroger, Burkhard  
 Schroder, Hartwig  
 Zelder, Oskar  
 Haberhauer, Gregor  
 Kim, Jun-Won  
 Lee, Heung-Schick  
 Hwang, Byung-Joon

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Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg  
 210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile  
 225 230 235 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn  
 245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly  
 260 265 270

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 Leu Thr Ile Pro Phe  
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gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163  
 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu  
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gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211  
 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp  
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cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct 259  
 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala  
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gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat 307  
 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp  
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tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg 355  
 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val  
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cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403  
 Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr  
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 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu  
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cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499  
 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro  
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gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547  
 Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala  
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 Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr  
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 Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr  
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 Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val  
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ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct 787  
 Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala  
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gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt 835  
 Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val  
 230 235 240 245

cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc 883  
 Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu  
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acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc 925  
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<213> Corynebacterium glutamicum

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 35 40 45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser  
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Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met  
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Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly  
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Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg  
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His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val  
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Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn  
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Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu  
145 150 155 160

Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu  
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Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn  
180 185 190

Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val  
195 200 205

Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val  
210 215 220

Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr  
225 230 235 240

Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp  
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Val Gln Ile  
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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123  
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cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219  
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 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

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 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
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atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
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 Ala Leu Phe  
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&lt;211&gt; 456

&lt;212&gt; PRT

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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45

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 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
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 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365

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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643  
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr  
170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691  
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser  
185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739  
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys  
200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
215 220 225

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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
230 235 240 245

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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
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265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
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Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
295 300 305

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310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123  
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171  
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala

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 375 380 385  
 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
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 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
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 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
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002221 0999760



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Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
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Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
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Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe
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Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe
		275					280					285			
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
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Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
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Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
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Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile
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Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
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Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
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Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
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Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly						
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ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg  163

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Pro	Asp	Thr	Phe	Phe	Leu	Leu	Arg	Leu	Ala	Thr	Arg	Ser	Arg	Ala	His		
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Ala	Ile	Ala	Gly	Val	Ala	Gly	Ile	Val	Thr	Gly	Leu	Thr	Val	Trp	Val		
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Ile	Leu	Gly	Ile	Ile	Gln	Leu	Val	Gly	Gly	Thr	Tyr	Leu	Ser	Phe	Ile		
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Gln	Phe	Arg	Phe	Asn	Ala	Asp	Ala	Arg	Pro	Ile	Pro	Asp	Ala	Val	Glu		
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ctg	tca	aac	cct	aaa	gtt	gtc	atg	tac	ttc	gcg	gca	att	ctg	gct	ccg	547	
Leu	Ser	Asn	Pro	Lys	Val	Val	Met	Tyr	Phe	Ala	Ala	Ile	Leu	Ala	Pro		
				135					140					145			
ttg	atg	cca	gcg	cac	cca	tca	ccg	gtg	ctg	gcg	ttc	tct	atc	atc	gtg	595	
Leu	Met	Pro	Ala	His	Pro	Ser	Pro	Val	Leu	Ala	Phe	Ser	Ile	Ile	Val		
				150					155					160			
165																	
gcg	att	tta	gtg	cag	acc	ttt	gtt	acc	ttc	tct	gct	gtg	tgc	ctc	att	643	
Ala	Ile	Leu	Val	Gln	Thr	Phe	Val	Thr	Phe	Ser	Ala	Val	Cys	Leu	Ile		
				170					175					180			
gtc	tct	acg	gag	cgt	gtg	cgc	aaa	gca	atg	ctg	cgt	gca	ggt	ccc	tgg	691	
Val	Ser	Thr	Glu	Arg	Val	Arg	Lys	Ala	Met	Leu	Arg	Ala	Gly	Pro	Trp		
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Phe	Asp	Leu	Leu	Ala	Gly	Val	Val	Phe	Leu	Val	Val	Gly	Val	Thr	Leu		
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ctg	tat	gaa	ggc	ctg	acc	ggt	tta	ctc	ggg	taaaggc	ata	aaaaatgg				789	
Leu	Tyr	Glu	Gly	Leu	Thr	Gly	Leu	Leu	Gly								
				215					220								
225																	
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Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly  
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Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu  
50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr  
65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu  
85 90 95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile  
100 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln  
115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala  
130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala  
145 150 155 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser  
165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu  
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<223> RXC01796

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Leu Leu Leu Gly Gly



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gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg      884
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Asp	Gln	Thr	Gln 20	Ile	Glu	Ser	Gly	Glu 25	Ser	Thr	Gly	Ala	Gly 30	Asp	Phe
Asp	His	Cys 35	Gln	Thr	Gly	Ala	Asp 40	Ala	Asn	Ala	Ser	Asp 45	Asp	Cys	Arg
Leu	Tyr 50	Tyr	Thr	Ser	Phe	Ser 55	Val	Asn	Glu	Met	Trp 60	Gln	Thr	Leu	Leu
Pro 65	Ala	Gln	Ala	Gly	Ile 70	Glu	Tyr	Thr	Glu	Pro 75	Thr	Leu	Thr	Leu	Phe 80
Lys	Asn	Ser	Thr	Gln 85	Thr	Gly	Cys	Gly	Phe 90	Ala	Ser	Ala	Ser	Thr 95	Gly
Pro	Phe	Tyr	Cys 100	Pro	Ser	Asp	Gln	Asp 105	Ala	Tyr	Phe	Asp	Leu 110	Thr	Phe
Phe	Asp	Gln 115	Met	Arg	Gln	Phe	Gly 120	Ala	Glu	Asn	Ala	Pro 125	Leu	Ala	Gln
Met	Tyr 130	Ile	Val	Ala	His	Glu 135	Tyr	Gly	His	His	Val 140	Gln	Asn	Leu	Glu
Gly 145	Thr	Leu	Gly	Leu	Ser 150	Asn	Tyr	Asn	Asp	Pro 155	Gly	Ala	Asp	Ser	Asn 160
Ala	Val	Lys	Ile 165	Glu	Leu	Gln	Ala	Asp	Cys 170	Tyr	Ala	Gly	Ile	Trp 175	Ala
Asn	His	Ser	Ser 180	Glu	Gly	Pro	Asp	Pro 185	Leu	Leu	Gln	Pro	Ile 190	Thr	Glu
Ser	Glu	Leu 195	Asp	Ser	Ala	Leu	Leu 200	Ala	Ala	Ser	Ala	Val 205	Gly	Asp	Asp
Asn	Ile 210	Gln	Gln	Arg	Ser	Gly 215	Gly	Asp	Val	Asn	Pro 220	Glu	Ser	Trp	Thr
His 225	Gly	Ser	Ser	Gln	Gln 230	Arg	Lys	Asp	Ala	Phe 235	Leu	Ala	Gly	Tyr	Asn 240
Thr	Gly	Gln	Met	Ser 245	Ala	Cys	Asp	Phe	Leu 250	Gly	Arg	Gly	Val	Tyr 255	Asn

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																																
Population (millions)	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9	10.0	10.1	10.2	10.3	10.4	10.5	10.6	10.7	10.8	10.9	11.0	11.1	11.2	11.3	11.4	11.5	11.6	11.7	11.8	11.9	12.0	12.1	12.2	12.3	12.4	12.5	12.6	12.7	12.8	12.9	13.0	13.1	13.2	13.3	13.4	13.5	13.6	13.7	13.8	13.9	14.0	14.1	14.2	14.3	14.4	14.5	14.6	14.7	14.8	14.9	15.0	15.1	15.2	15.3	15.4	15.5	15.6	15.7	15.8	15.9	16.0	16.1	16.2	16.3	16.4	16.5	16.6	16.7	16.8	16.9	17.0	17.1	17.2	17.3	17.4	17.5	17.6	17.7	17.8	17.9	18.0	18.1	18.2	18.3	18.4	18.5	18.6	18.7	18.8	18.9	19.0	19.1	19.2	19.3	19.4	19.5	19.6	19.7	19.8	19.9	20.0	20.1	20.2	20.3	20.4	20.5	20.6	20.7	20.8	20.9	21.0	21.1	21.2	21.3	21.4	21.5	21.6	21.7	21.8	21.9	22.0	22.1	22.2	22.3	22.4	22.5	22.6	22.7	22.8	22.9	23.0	23.1	23.2	23.3	23.4	23.5	23.6	23.7	23.8	23.9	24.0	24.1	24.2	24.3	24.4	24.5	24.6	24.7	24.8	24.9	25.0	25.1	25.2	25.3	25.4	25.5	25.6	25.7	25.8	25.9	26.0	26.1	26.2	26.3	26.4	26.5	26.6	26.7	26.8	26.9	27.0	27.1	27.2	27.3	27.4	27.5	27.6	27.7	27.8	27.9	28.0	28.1	28.2	28.3	28.4	28.5	28.6	28.7	28.8	28.9	29.0	29.1	29.2	29.3	29.4	29.5	29.6	29.7	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4

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 Val Ser Arg Ile Tyr  
 1 5  
 gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163  
 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val  
 10 15 20  
 gat gca gtc aaa gcc ggt cag ctg gtt gtc ctt ccc acg gat acc ctt 211  
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu  
 25 30 35  
 tat gga ctg ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259  
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu  
 40 45 50  
 ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctg gtc 307  
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val  
 55 60 65  
 ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355  
 Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln  
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 105 110 115  
 acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499  
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu  
 120 125 130  
 cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547  
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His  
 135 140 145  
 act cct cca acc acc gtg ctg gag gct cgt cag cag ctg aac caa aat 595  
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Pro	Thr	Asp	Thr	Leu	Tyr	Gly	Leu	Gly	Cys	Asp	Ala	Phe	Asn	Asn	Glu	
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Ser	Tyr	Ser	Ala	Gln	Ala	Lys	Ala	Leu	Val	Glu	Ala	Phe	Trp	Pro	Gly	
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Leu	Ala	Thr	Pro	Ser	Thr	Ile	Val	Asp	Ile	Ser	Gly	Pro	Ala	Pro	Lys	
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Met Ser Thr Glu Asp  
1 5  
att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163  
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val  
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cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211  
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu  
25 30 35  
gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259  
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val  
40 45 50  
cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag 307  
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys  
55 60 65  
att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag 355  
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys  
70 75 80 85  
atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa 403  
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu  
90 95 100  
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Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly  
105 110 115  
gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc 499  
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser  
120 125 130  
cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac 547  
His Ala Lys Cys Pro Val Val Val Arg Glu Asp Ser Ala Val Asn  
135 140 145  
gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595  
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Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
          50                        55                60
Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
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Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile

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[illegible]

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90

95

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100 105 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser  
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Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu  
130 135 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly  
145 150 155 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala  
165 170 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met  
180 185 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln  
195 200 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg  
210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile  
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Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn  
245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly  
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<223> RXC00552

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Val Ala Thr Ser Lys  
1 5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163  
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val

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10

15

20

cag	ctg	tgg	cag	cgt	gag	ctc	tgc	gag	tca	ctg	aat	ctt	cgt	ggc	cgc	211
Gln	Leu	Trp	Gln	Arg	Glu	Leu	Cys	Glu	Ser	Leu	Asn	Leu	Arg	Gly	Arg	
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Ile	Leu	Ile	Ser	Thr	His	Gly	Ile	Asn	Gly	Thr	Val	Gly	Gly	Asp	Ile	
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Asp	Asp	Cys	Lys	Ala	Tyr	Ile	Lys	Lys	Thr	Arg	Glu	Tyr	Pro	Gly	Phe	
	55					60					65					
aac	cgc	atg	cag	ttt	aag	tgg	tcc	gag	ggt	ggc	gct	gag	gat	ttc	cca	355
Asn	Arg	Met	Gln	Phe	Lys	Trp	Ser	Glu	Gly	Gly	Ala	Glu	Asp	Phe	Pro	
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Lys	Leu	Ser	Val	Lys	Val	Arg	Asp	Glu	Ile	Val	Ala	Phe	Gly	Ala	Pro	
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gat	gag	ctc	aaa	gtg	gat	gaa	aac	ggc	gtc	gtc	ggt	ggc	ggc	gtt	cac	451
Asp	Glu	Leu	Lys	Val	Asp	Glu	Asn	Gly	Val	Val	Gly	Gly	Gly	Val	His	
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Leu	Lys	Pro	Gln	Gln	Val	Asn	Glu	Leu	Val	Glu	Ala	Arg	Gly	Asp	Glu	
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gtt	gtg	ttc	ttt	gac	ggc	cgc	aac	gca	atg	gaa	gcc	cag	atc	ggc	aag	547
Val	Val	Phe	Phe	Asp	Gly	Arg	Asn	Ala	Met	Glu	Ala	Gln	Ile	Gly	Lys	
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Phe	Lys	Asp	Ala	Val	Val	Pro	Asp	Val	Glu	Thr	Thr	His	Asp	Phe	Ile	
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Ala	Glu	Ile	Glu	Ser	Gly	Lys	Tyr	Asp	Asp	Leu	Lys	Asp	Lys	Pro	Val	
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Val	Thr	Tyr	Cys	Thr	Gly	Gly	Ile	Arg	Cys	Glu	Ile	Leu	Ser	Ser	Leu	
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Met	Ile	Asn	Arg	Gly	Phe	Lys	Glu	Val	Tyr	Gln	Ile	Asp	Gly	Gly	Ile	
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Val	Arg	Tyr	Gly	Glu	Gln	Phe	Gly	Asn	Lys	Gly	Leu	Trp	Glu	Gly	Ser	
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ctc	tac	gtt	ttc	gat	aag	cgc	atg	cat	atg	gaa	ttc	ggc	gag	gat	tac	835
Leu	Tyr	Val	Phe	Asp	Lys	Arg	Met	His	Met	Glu	Phe	Gly	Glu	Asp	Tyr	
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Lys	Glu	Val	Gly	His	Cys	Ile	His	Cys	Asp	Thr	Pro	Thr	Asn	Lys	Phe	
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 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys  
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cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979  
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg  
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tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc 1027  
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 Val Thr Ser  
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&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 22

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Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr  
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Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg  
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Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly  
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Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val  
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Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val  
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Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu  
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Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu  
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Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr  
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Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu  
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Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu  
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Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln

002222 09944660 122000

195 200 205

Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly  
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Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu  
225 230 235 240

Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr  
245 250 255

Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu  
260 265 270

Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His  
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Val Ala Leu Val Val  
1 5

cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac 163  
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn  
10 15 20

gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg 211  
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val  
25 30 35

gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt 259  
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu  
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gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc 307  
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu  
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ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355  
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile  
70 75 80 85

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 90 95 100

gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451  
 Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr  
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cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt 499  
 Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val  
 120 125 130

gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547  
 Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu  
 135 140 145

ggt cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg 595  
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Leu Ala Ala Ala Leu  
 150 155 160 165

aac gct gat gtg tgt gag att tac tcg gac gtt gac ggt gtg tat acc 643  
 Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val Asp Gly Val Tyr Thr  
 170 175 180

gct gac ccg cgc atc gtt cct aat gca cag aag ctg gaa aag ctc agc 691  
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ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc tcc aag att ttg gtg 739  
 Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly Ser Lys Ile Leu Val  
 200 205 210

ctg cgc agt gtt gaa tac gct cgt gca ttc aat gtg cca ctt cgc gta 787  
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cgc tcg tct tat agt aat gat ccc ggc act ttg att gcc ggc tct atg 835  
 Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu Ile Ala Gly Ser Met  
 230 235 240 245

gag gat att cct gtg gaa gaa gca gtc ctt acc ggt gtc gca acc gac 883  
 Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp  
 250 255 260

aag tcc gaa gcc aaa gta acc gtt ctg ggt att tcc gat aag cca ggc 931  
 Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly  
 265 270 275

gag gct gcg aag gtt ttc cgt gcg ttg gct gat gca gaa atc aac att 979  
 Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile  
 280 285 290

gac atg gtt ctg cag aac gtc tct tct gta gaa gac ggc acc acc gac 1027  
 Asp Met Val Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp  
 295 300 305

atc acc ttc acc tgc cct cgt tcc gac ggc cgc cgc gcg atg gag atc 1075  
 Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg Arg Ala Met Glu Ile  
 310 315 320 325

ttg aag aag ctt cag gtt cag ggc aac tgg acc aat gtg ctt tac gac 1123

002221" 0999460

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gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct ggc atg aag tct cac 1171  
 Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His  
 345 350 355

cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg 1219  
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val  
 360 365 370

aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc 1267  
 Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile  
 375 380 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc 1315  
 Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe  
 390 395 400 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc 1363  
 Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg  
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 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
 145 150 155 160

002221-00000000

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
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 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
 180 185 190  
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 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220  
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240  
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255  
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
 260 265 270  
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
 275 280 285  
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 290 295 300  
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320  
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335  
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 340 345 350  
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 355 360 365  
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380  
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 385 390 395 400  
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
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 Ala Gly Thr Gly Arg  
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<210> 25

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

002221 09091260



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 Met Thr Thr Ile Ala  
 1 5

gtt gtt ggt gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg 163  
 Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu  
 10 15 20

gaa gag cgc aat ttc cca gct gac act gtt cgt ttc ttt gct tcc cca 211  
 Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro  
 25 30 35

cgt tcc gca ggc cgt aag att gaa ttc cgt ggc acg gaa atc gag gta 259  
 Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val  
 40 45 50

gaa gac att act cag gca acc gag gag tcc ctc aag gac atc gac gtt 307  
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ttc gct gct gca ggc gcg act gtt gtg gat aac tct tct gct tgg cgc 403  
 Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg  
 90 95 100

aag gac gac gag gtt cca cta atc gtc tct gag gtg aac cct tcc gac 451  
 Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp  
 105 110 115

aag gat tcc ctg gtc aag ggc att att gcg aac cct aac tgc acc acc 499  
 Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr  
 120 125 130

atg gct gcg atg cca gtg ctg aag cca ctt cac gat gcc gct ggt ctt 547  
 Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu  
 135 140 145

gta aag ctt cac gtt tcc tct tac cag gct gtt tcc ggt tct ggt ctt 595  
 Val Lys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu  
 150 155 160 165

gca ggt gtg gaa acc ttg gca aag cag gtt gct gca gtt gga gac cac 643  
 Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His  
 170 175 180

aac gtt gag ttc gtc cat gat gga cag gct gct gac gca ggc gat gtc 691  
 Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val  
 185 190 195

gga cct tat gtt tca cca atc gct tac aac gtg ctg cca ttc gcc gga 739  
 Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly  
 200 205 210

002221 0994760

aac ctc gtc gat gac ggc acc ttc gaa acc gat gaa gag cag aag ctg 787  
 Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp Glu Glu Gln Lys Leu  
 215 220 225  
  
 cgc aac gaa tcc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835  
 Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser  
 230 235 240 245  
  
 ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883  
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile  
 250 255 260  
  
 cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931  
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile  
 265 270 275  
  
 ttg ggt gcc got tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt 979  
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu  
 280 285 290  
  
 gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac 1027  
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp  
 295 300 305  
  
 tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac 1075  
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp  
 310 315 320 325  
  
 aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg 1123  
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 26

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 35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
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Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
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Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
 85 90 95

002227 0999460 12200

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
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Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn  
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His  
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val  
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala  
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala  
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val  
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp  
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro  
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly  
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp  
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp  
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly  
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu  
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile  
325 330 335

Gln Ile Ala Glu Leu Leu Val Lys  
340

&lt;210&gt; 27

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (69)..(608)

&lt;223&gt; RXA02843

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 acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158  
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp  
 15 20 25 30  
 cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206  
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val  
 35 40 45  
 acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254  
 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr  
 50 55 60  
 gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302  
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val  
 65 70 75  
 ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350  
 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn  
 80 85 90  
 aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398  
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala  
 95 100 105 110  
 ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446  
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser  
 115 120 125  
 gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494  
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val  
 130 135 140  
 cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542  
 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp  
 145 150 155  
 ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590  
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr  
 160 165 170  
 ctc ggc gct tcc atg gtt 608  
 Leu Gly Ala Ser Met Val  
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&lt;210&gt; 28

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 28

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly  
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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser  
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002221-099460



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tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac 355  
 Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp  
 70 75 80 85

aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc 403  
 Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr  
 90 95 100

gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc 451  
 Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr  
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gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc 547  
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 135 140 145

gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag 595  
 Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu  
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cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc 643  
 Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile  
 170 175 180

aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg 691  
 Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu  
 185 190 195

ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct 739  
 Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala  
 200 205 210

gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa 787  
 Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu  
 215 220 225

ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att 835  
 Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile  
 230 235 240 245

cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc 883  
 Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg  
 250 255 260

gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac 931  
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 265 270 275

ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc 979  
 Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala  
 280 285 290

ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc 1027

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<213> Corynebacterium glutamicum

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Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
          35          40          45
Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
  50          55          60
Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
  65          70          75          80
Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
          85          90          95
Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
          100          105          110
His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
          115          120          125
Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
          130          135          140
Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
          145          150          155          160
Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
          165          170          175

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Figure 1 consists of 12 bar charts, labeled (a) through (l), each representing a different demographic or attitudinal variable. Each chart has two bars: a solid black bar representing the percentage of respondents in the sample and a white bar with a black outline representing the percentage of the total population. The y-axis for all charts is labeled 'Percentage' and ranges from 0 to 100. The x-axis for each chart is labeled with the variable name. The variables are: (a) Age, (b) Sex, (c) Education, (d) Income, (e) Employment, (f) Home ownership, (g) Political affiliation, (h) Party affiliation, (i) Party identification, (j) Party loyalty, (k) Party support, and (l) Party preference. In general, the sample percentages are very close to the population percentages, indicating a representative sample.

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser  
 180 185 190  
 Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile  
 195 200 205  
 Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly  
 210 215 220  
 Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val  
 225 230 235 240  
 Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg  
 245 250 255  
 Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu  
 260 265 270  
 Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp  
 275 280 285  
 Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly  
 290 295 300  
 Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp  
 305 310 315 320  
 Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe  
 325 330 335  
 Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro  
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 355 360 365  
 Glu

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 Met Ala Ser Ala Thr  
 1 5  
 ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163  
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly  
 10 15 20

0974660 "12300





Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His  
 265 270 275

ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979  
 Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu  
 280 285 290

agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg 1027  
 Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu  
 295 300 305

tac acc gct taaggccac acctcatgac tga 1059  
 Tyr Thr Ala  
 310

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 20 25 30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser  
 35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu  
 50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly  
 65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala  
 85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr  
 100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala  
 115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val  
 130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly  
 145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg  
 165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys  
 180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly  
 195 200 205

002221 09997260

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr  
 210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala  
 225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly  
 245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys  
 260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val  
 275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile  
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Val Asp Glu Phe Leu Tyr Thr Ala  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00863

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gtttgaaaaa ctcttcgccc cacgaaaatg aaggagcata atg gga atc aag gtt 115  
 Met Gly Ile Lys Val  
 1 5

ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163  
 Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala  
 10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211  
 Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp  
 25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259  
 Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp  
 40 45 50

ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307  
 Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn  
 55 60 65

aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt 355  
 Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg  
 70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403  
 Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val

0946560 "123000

100

cta ggc ctg taaaggctca tttcagcagc ggg 867  
Leu Gly Leu

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<400> 34
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  1                               5          10          15

Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
      20          25          30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
      35          40          45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
      50          55          60

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Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly  
 65 70 75 80  
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys  
 85 90 95  
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val  
 100 105 110  
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala  
 115 120 125  
 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly  
 130 135 140  
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala  
 145 150 155 160  
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser  
 165 170 175  
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser  
 180 185 190  
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr  
 195 200 205  
 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly  
 210 215 220  
 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val  
 225 230 235 240  
 Gly Leu Glu His Tyr Leu Gly Leu  
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 <223> RXA00864

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 Val Ala Glu Gln Val  
 1 5  
 aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163  
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala  
 10 15 20  
 gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag 211  
 Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu  
 25 30 35

002227-09994260

ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259  
 Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg  
 40 45 50

act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac 307  
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His  
 55 60 65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 355  
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile  
 70 75 80 85

tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403  
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe  
 90 95 100

tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg 451  
 Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val  
 105 110 115

gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg 499  
 Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met  
 120 125 130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg 547  
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala  
 135 140 145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag 595  
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys  
 150 155 160 165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc 643  
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser  
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691  
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly  
 185 190 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta 739  
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val  
 200 205 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787  
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp  
 215 220 225

ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg 835  
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro  
 230 235 240 245

tat gtc atg gac ttt taacgcaaag ctacaccca cga 873  
 Tyr Val Met Asp Phe  
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<210> 36  
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09746660-12200

<213> Corynebacterium glutamicum

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20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
195 200 205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe  
245 250

<210> 37

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA02843

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tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110  
 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser  
 1 5 10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158  
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp  
 15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206  
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val  
 35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254  
 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr  
 50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302  
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val  
 65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350  
 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn  
 80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398  
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala  
 95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446  
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser  
 115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494  
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val  
 130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542  
 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp  
 145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590  
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr  
 160 165 170

ctc ggc gct tcc atg gtt 608  
 Leu Gly Ala Ser Met Val  
 175 180

&lt;210&gt; 38

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly  
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0946660 13300



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<220>  
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<223> RXN00355
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ggtcctgatg aaagagatgt cccatgaatca tcattctaagt atg cat ctc ggt aag 115
Met His Leu Gly Lys
1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259

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<213> Corynebacterium glutamicum
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			20					25					30			
Asn	Leu	Gly	Arg	Ser	Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	
		35					40					45				
Asp	Leu	Val	Gly	Ile	Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	
	50					55					60					
Pro	Val	Phe	Asp	Val	Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	
65					70					75					80	
Val	Leu	Phe	Leu	Cys	Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	
				85					90					95		
Pro	Lys	Phe	Ala	Gln	Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	
			100					105					110			
Arg	Asp	Ile	Pro	Arg	His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	
		115					120					125				
Ala	Gly	Asn	Val	Ala	Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	
	130					135					140					
Ser	Ile	Asn	Arg	Val	Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	
145					150					155					160	
His	Thr	Phe	Trp	Gly	Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	
				165					170					175		
Arg	Arg	Ile	Pro	Gly	Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	
			180					185					190			
Glu	Asp	Ala	Leu	Glu	Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	
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<223> FRXA00352
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															atg cat ctc ggt aag	115
															Met His Leu Gly Lys	
															1 5	
ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg															163	
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met																
															10 15 20	
acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc															211	
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser																
															25 30 35	
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc															259	
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile																
															40 45 50	
ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc															307	
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val																
															55 60 65	

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc 355  
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys  
 70 75 80 85  
  
 atg ggc tcc gcc acc gac atc oct gag cag gca cca aag ttc gcg cag 403  
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln  
 90 95 100  
  
 ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc 451  
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg  
 105 110 115  
  
 cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca 499  
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala  
 120 125 130  
  
 ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc 547  
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val  
 135 140 145  
  
 tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc 595  
 Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly  
 150 155 160 165  
  
 cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc 643  
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly  
 170 175 180  
  
 gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa 691  
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu  
 185 190 195  
  
 aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac 739  
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His  
 200 205 210  
  
 aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc 787  
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile  
 215 220 225  
  
 gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835  
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val  
 230 235 240 245  
  
 gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc 883  
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly  
 250 255 260  
  
 atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc 931  
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe  
 265 270 275  
  
 aac cac acc gtg gaa tac atc ctc aag 958  
 Asn His Thr Val Glu Tyr Ile Leu Lys  
 280 285

<210> 42  
 <211> 286  
 <212> PRT

002227"09994260

<400> 42

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys  
275 280 285

<212> DNA

Economic Indicators	
GDP (billion \$)	1,200
Per capita GDP (\$)	1,200
Unemployment (%)	5.0
Inflation (%)	2.0
Interest Rate (%)	5.0
Exchange Rate (\$/£)	1.50
Trade Balance (\$ billion)	100
Government Budget (\$ billion)	50
Public Debt (\$ billion)	200
Foreign Reserves (\$ billion)	150
Central Bank Assets (\$ billion)	100
Central Bank Liabilities (\$ billion)	100
Money Supply (\$ billion)	1,000
Banking Sector Assets (\$ billion)	800
Banking Sector Liabilities (\$ billion)	800
Insurance Sector Assets (\$ billion)	500
Insurance Sector Liabilities (\$ billion)	500
Real Estate Sector Assets (\$ billion)	300
Real Estate Sector Liabilities (\$ billion)	300
Non-Financial Sector Assets (\$ billion)	200
Non-Financial Sector Liabilities (\$ billion)	200
Financial Sector Assets (\$ billion)	1,000
Financial Sector Liabilities (\$ billion)	1,000
Government Assets (\$ billion)	100
Government Liabilities (\$ billion)	100
Private Assets (\$ billion)	900
Private Liabilities (\$ billion)	900
Total Assets (\$ billion)	2,000
Total Liabilities (\$ billion)	2,000
Equity (\$ billion)	1,000
Debt (\$ billion)	1,000
Capital (\$ billion)	500
Reserves (\$ billion)	500
Provisions (\$ billion)	50
Other (\$ billion)	50

<213> Corynebacterium glutamicum

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<222> (1) .. (1377)

<223> RXA00972

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aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat 96  
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn  
20 25 30

gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg 144  
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu  
35 40 45

cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag 192  
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu  
50 55 60

gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga 240  
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly  
65 70 75 80

cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att 288  
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile  
85 90 95

gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc 336  
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile  
100 105 110

aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc 384  
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile  
115 120 125

acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt 432  
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val  
130 135 140

caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa 480  
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu  
145 150 155 160

ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg 528  
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu  
165 170 175

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc 576  
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala  
180 185 190

act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc 624  
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser  
195 200 205

gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg 672

The distribution of the number of children in the family	
Number of children	Percentage of families
0	1.2
1	10.8
2	28.5
3	24.3
4	15.7
5	10.2
6	4.5
7	2.1
8	0.8
9	0.3
10	0.1
11	0.1
12	0.1
13	0.1
14	0.1
15	0.1
16	0.1
17	0.1
18	0.1
19	0.1
20	0.1
21	0.1
22	0.1
23	0.1
24	0.1
25	0.1
26	0.1
27	0.1
28	0.1
29	0.1
30	0.1
31	0.1
32	0.1
33	0.1
34	0.1
35	0.1
36	0.1
37	0.1
38	0.1
39	0.1
40	0.1
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 Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His  
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 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His  
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 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met  
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 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly  
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09746660-12200



450

455

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1400

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<212> PRT  
<213> Corynebacterium glutamicum

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Ala	Val	Arg	Gln	Glu	Asp	Gly	Val	Val	Thr	Val	Ala	Gly	Val	Pro	Leu	
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Asp	Asp	Phe	Arg	Ser	Arg	Cys	Arg	Asp	Met	Ala	Thr	Ala	Phe	Gly	Gly	
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Pro	Gly	Asn	Val	His	Tyr	Ala	Ser	Lys	Ala	Phe	Leu	Thr	Lys	Thr	Ile	
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Ala	Arg	Trp	Val	Asp	Glu	Glu	Gly	Leu	Ala	Leu	Asp	Ile	Ala	Ser	Ile	
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Asn	Glu	Leu	Gly	Ile	Ala	Leu	Ala	Ala	Gly	Phe	Pro	Ala	Ser	Arg	Ile	
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Thr	Ala	His	Gly	Asn	Asn	Lys	Gly	Val	Glu	Phe	Leu	Arg	Ala	Leu	Val	
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Gln	Asn	Gly	Val	Gly	His	Val	Val	Leu	Asp	Ser	Ala	Gln	Glu	Leu	Glu	
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Leu	Leu	Asp	Tyr	Val	Ala	Ala	Gly	Glu	Gly	Lys	Ile	Gln	Asp	Val	Leu	
				165					170					175		
Ile	Arg	Val	Lys	Pro	Gly	Ile	Glu	Ala	His	Thr	His	Glu	Phe	Ile	Ala	
			180					185					190			
Thr	Ser	His	Glu	Asp	Gln	Lys	Phe	Gly	Phe	Ser	Leu	Ala	Ser	Gly	Ser	
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Ala	Phe	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Asn	Ala	Glu	Asn	Leu	Asn	Leu	
	210					215					220					
Val	Gly	Leu	His	Cys	His	Val	Gly	Ser	Gln	Val	Phe	Asp	Ala	Glu	Gly	
225					230					235					240	
Phe	Lys	Leu	Ala	Ala	Glu	Arg	Val	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	His	
				245					250					255		
Ser	Glu	Leu	Gly	Val	Ala	Leu	Pro	Glu	Leu	Asp	Leu	Gly	Gly	Gly	Tyr	
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 Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp  
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acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg 1075  
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 Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe  
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 Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu  
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gat tgg atc cgt tat caa tcc gct aaa tct gcg act tca gcc ggg tat 1555  
 Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr  
 470 475 480 485

gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg 1603  
 Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro  
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gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa 1747  
Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu  
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Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu  
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Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile  
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Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala  
585 590 595

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Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg  
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cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att 1987  
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Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His  
630 635 640 645

caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac 2083  
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp  
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&lt;211&gt; 666

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&lt;213&gt; Corynebacterium glutamicum

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Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly  
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Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr  
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Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile  
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Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro  
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 Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val  
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 Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu  
 115 120 125  
 Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro  
 130 135 140  
 Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly  
 145 150 155 160  
 Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp  
 165 170 175  
 Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr  
 180 185 190  
 Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp  
 195 200 205  
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr  
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 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro  
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 260 265 270  
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 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg  
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 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu  
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 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile  
 355 360 365  
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala  
 370 375 380  
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala  
 385 390 395 400

09746660-12200

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.4	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.6	0.5	0	1
Sleep quality	0.7	0.4	0	1
Work satisfaction	0.6	0.5	0	1
Life satisfaction	0.7	0.4	0	1
Depression score	10.5	5.5	0	30
Anxiety score	12.5	6.5	0	35
Quality of life score	75.5	15.5	30	100

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Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
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Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
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Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
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atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt 355
Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu
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Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr
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ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg 499
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg
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cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg 547
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala
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gga tgt gaa gta gta gaa ctt gga acc atg gcg cac ttg gcc att gca 595
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
                        150                155                160                165

acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg 643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp
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gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
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cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val
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gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg 883  
 Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met  
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gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc 980  
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Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln  
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Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala  
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Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser  
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr  
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu  
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg  
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His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp  
 165 170 175

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Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys  
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Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val  
195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu  
210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala  
225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro  
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser  
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Arg Pro  
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<223> RXA00241

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Val Asn Thr Gln Ser  
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gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163  
Asp Ser Ala Gly Ser Gln Gly Ala Ala Thr Ser Arg Thr Val Ser  
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att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga 211  
Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly  
25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259  
Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala  
40 45 50

atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307  
Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala  
55 60 65

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Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly  
70 75 80 85

00222T"0999460

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 105 110 115

gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc 499  
 Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser  
 120 125 130

caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg 547  
 Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp  
 135 140 145

ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg 595  
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 170 175 180

atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat 691  
 Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp  
 185 190 195

tta tgg gcg cgt gat ggt ggc gtg ggc agc att ttt gat cag gtg cgc 739  
 Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg  
 200 205 210

ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca 787  
 Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala  
 215 220 225

tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct 835  
 Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala  
 230 235 240 245

acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct 883  
 Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser  
 250 255 260

tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca 931  
 Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro  
 265 270 275

gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt 979  
 Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly  
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gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat 1027  
 Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr  
 295 300 305

gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg 1075  
 Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met  
 310 315 320 325

09746660-123200



Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly  
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 Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro  
 65 70 75 80  
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp  
 85 90 95  
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile  
 100 105 110  
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr  
 115 120 125  
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val  
 130 135 140  
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser  
 145 150 155 160  
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro  
 165 170 175  
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu  
 180 185 190  
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile  
 195 200 205  
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile  
 210 215 220  
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser  
 225 230 235 240  
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu  
 245 250 255  
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu  
 260 265 270  
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 275 280 285  
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser  
 290 295 300  
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu  
 305 310 315 320  
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile  
 325 330 335  
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val  
 340 345 350  
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val  
 355 360 365

09745660-12200

Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe  
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Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr  
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His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser  
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Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val  
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Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe  
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Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg  
450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val  
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Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn  
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Gly Ser Leu Ser Leu  
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<223> RXA01394
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Met Glu Ile Phe Ile  
1 5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163  
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Ser Ile Gly Pro Gln  
10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211  
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala  
25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259  
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly  
40 45 50

acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307  
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20 25 30  
Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe  
35 40 45  
Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender	
Male	50.0
Female	50.0
Education (years)	12.0 ± 1.0
Marital status	
Married	60.0
Single	40.0
Occupation	
Retired	60.0
Working	40.0
Income (USD/month)	1,500.0 ± 200.0
Health status	
Good	60.0
Poor	40.0
Smoking status	
Smoker	30.0
Non-smoker	70.0
Alcohol consumption	
Drinker	20.0
Non-drinker	80.0
Comorbidities	
Hypertension	40.0
Diabetes	30.0
Cholesterol	20.0
Arthritis	10.0
Depression	10.0
Medication use	
Yes	60.0
No	40.0

50					55					60					
Pro 65	Ile	Val	Leu	Asp	Ile 70	Met	Arg	Trp	Gly	Gly 75	Ile	Ala	Tyr	Leu	Leu 80
Trp	Phe	Ala	Val	Met 85	Ala	Ala	Lys	Asp	Ala 90	Met	Thr	Asn	Lys	Val 95	Glu
Ala	Pro	Gln	Ile 100	Ile	Glu	Glu	Thr	Glu 105	Pro	Thr	Val	Pro	Asp 110	Asp	Thr
Pro	Leu	Gly 115	Gly	Ser	Ala	Val	Ala 120	Thr	Asp	Thr	Arg	Asn 125	Arg	Val	Arg
Val	Glu 130	Val	Ser	Val	Asp	Lys 135	Gln	Arg	Val	Trp	Val 140	Lys	Pro	Met	Leu
Met 145	Ala	Ile	Val	Leu	Thr 150	Trp	Leu	Asn	Pro	Asn 155	Ala	Tyr	Leu	Asp	Ala 160
Phe	Val	Phe	Ile	Gly 165	Gly	Val	Gly	Ala	Gln 170	Tyr	Gly	Asp	Thr	Gly 175	Arg
Trp	Ile	Phe	Ala 180	Ala	Gly	Ala	Phe	Ala 185	Ala	Ser	Leu	Ile	Trp 190	Phe	Pro
Leu	Val	Gly 195	Phe	Gly	Ala	Ala	Ala 200	Leu	Ser	Arg	Pro	Leu 205	Ser	Ser	Pro
Lys 210	Val	Trp	Arg	Trp	Ile	Asn 215	Val	Val	Val	Ala	Val 220	Val	Met	Thr	Ala
Leu 225	Ala	Ile	Lys	Leu	Met 230	Leu	Met	Gly							

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Met Ser Thr Gly Leu
1 5

aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
10 15 20

gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
25 30 35

```

Figure 1 consists of 26 panels (a-z) showing the effect of the 12S mutation on various parameters in Arabidopsis. The parameters are listed on the left of each panel, and the genotypes (WT, 12S, 12S/12S) are compared. The y-axis for all panels is 'mg' (milligrams). The data is summarized in the following table:

Parameter	WT	12S	12S/12S
(a) Seed weight (mg)	~1.0	~1.0	~1.0
(b) Seed weight (mg)	~1.0	~1.0	~1.0
(c) Seed weight (mg)	~1.0	~1.0	~1.0
(d) Seed weight (mg)	~1.0	~1.0	~1.0
(e) Seed weight (mg)	~1.0	~1.0	~1.0
(f) Seed weight (mg)	~1.0	~1.0	~1.0
(g) Seed weight (mg)	~1.0	~1.0	~1.0
(h) Seed weight (mg)	~1.0	~1.0	~1.0
(i) Seed weight (mg)	~1.0	~1.0	~1.0
(j) Seed weight (mg)	~1.0	~1.0	~1.0
(k) Seed weight (mg)	~1.0	~1.0	~1.0
(l) Seed weight (mg)	~1.0	~1.0	~1.0
(m) Seed weight (mg)	~1.0	~1.0	~1.0
(n) Seed weight (mg)	~1.0	~1.0	~1.0
(o) Seed weight (mg)	~1.0	~1.0	~1.0
(p) Seed weight (mg)	~1.0	~1.0	~1.0
(q) Seed weight (mg)	~1.0	~1.0	~1.0
(r) Seed weight (mg)	~1.0	~1.0	~1.0
(s) Seed weight (mg)	~1.0	~1.0	~1.0
(t) Seed weight (mg)	~1.0	~1.0	~1.0
(u) Seed weight (mg)	~1.0	~1.0	~1.0
(v) Seed weight (mg)	~1.0	~1.0	~1.0
(w) Seed weight (mg)	~1.0	~1.0	~1.0
(x) Seed weight (mg)	~1.0	~1.0	~1.0
(y) Seed weight (mg)	~1.0	~1.0	~1.0
(z) Seed weight (mg)	~1.0	~1.0	~1.0



gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc 259  
 Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu  
 40 45 50

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta 307  
 Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu  
 55 60 65

gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc 355  
 Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu  
 70 75 80 85

atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg 403  
 Ile Ala Gly Val Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala  
 90 95 100

gaa gct gct gct tct gct ggc gca gac gcc ctt tta gtt gta act cct 451  
 Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro  
 105 110 115

tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca 499  
 Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala  
 120 125 130

att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt 547  
 Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly  
 135 140 145

cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa 595  
 Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu  
 150 155 160 165

tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca 643  
 Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala  
 170 175 180

gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat 691  
 Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp  
 185 190 195

gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att 739  
 Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile  
 200 205 210

tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca 787  
 Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr  
 215 220 225

agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa 835  
 Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys  
 230 235 240 245

cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg 883  
 Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu  
 250 255 260

gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga 931  
 Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg  
 265 270 275

ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa 979

002221 "0999760

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 280 285 290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccgaa aat 1026  
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 <213> Corynebacterium glutamicum

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 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr  
 50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly  
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr  
 85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu  
 100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu  
 115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu  
 130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met  
 145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys  
 165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala  
 180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly  
 195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu  
 210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg  
 225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu  
 245 250 255

002221 0994260

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn  
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu  
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Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  
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<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXS02021

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Met Ser Glu Asn Ile  
1 5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163  
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr  
10 15 20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211  
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln  
25 30 35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259  
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala  
40 45 50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307  
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp  
55 60 65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355  
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser  
70 75 80 85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403  
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu  
90 95 100

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Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu  
105 110 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499  
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro  
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002227" 09994460

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 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe  
 185 190 195  
 aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739  
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser  
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 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile  
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 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu  
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 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr  
 265 270 275  
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 280 285 290  
 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027  
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Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

002221 099466

35

40

45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val  
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 Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val  
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 Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu  
 85 90 95  
 Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His  
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 Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys  
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 Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg  
 130 135 140  
 Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met  
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 Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg  
 165 170 175  
 Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu  
 180 185 190  
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 195 200 205  
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&lt;211&gt; 1296

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&lt;221&gt; CDS

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&lt;223&gt; RXS02157

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				Met	Ser	Thr	Leu	Glu	
				1				5	

act	tgg	cca	cag	gtc	att	att	aat	acg	tac	ggc	acc	cca	cca	gtt	gag	163
Thr	Trp	Pro	Gln	Val	Ile	Ile	Asn	Thr	Tyr	Gly	Thr	Pro	Pro	Val	Glu	
			10						15					20		

ctg	gtg	tcc	ggc	aag	ggc	gca	acc	gtc	act	gat	gac	cag	ggc	aat	gtc	211
Leu	Val	Ser	Gly	Lys	Gly	Ala	Thr	Val	Thr	Asp	Asp	Gln	Gly	Asn	Val	
			25					30					35			

tac	atc	gac	ttg	ctc	gcg	ggc	atc	gca	gtc	aac	gcg	ttg	ggc	cac	gcc	259
Tyr	Ile	Asp	Leu	Leu	Ala	Gly	Ile	Ala	Val	Asn	Ala	Leu	Gly	His	Ala	
		40					45					50				

cac	cgc	gcg	atc	atc	gag	gcg	gtc	acc	aac	cag	atc	ggc	caa	ctt	ggc	307
His	Pro	Ala	Ile	Ile	Glu	Ala	Val	Thr	Asn	Gln	Ile	Gly	Gln	Leu	Gly	
	55					60					65					

cac	gtc	tca	aac	ttg	ttc	gca	tcc	agg	ccc	gtc	gtc	gag	gtc	gcc	gag	355
His	Val	Ser	Asn	Leu	Phe	Ala	Ser	Arg	Pro	Val	Val	Glu	Val	Ala	Glu	
	70				75				80					85		

gag	ctc	atc	aag	cgt	ttt	tcg	ctt	gac	gac	gcc	acc	ctc	gcc	gcg	caa	403
Glu	Leu	Ile	Lys	Arg	Phe	Ser	Leu	Asp	Asp	Ala	Thr	Leu	Ala	Ala	Gln	
			90						95					100		

acc	cgc	gtt	ttc	ttc	tgc	aac	tcg	ggc	gcc	gaa	gca	aac	gag	gct	gct	451
Thr	Arg	Val	Phe	Phe	Cys	Asn	Ser	Gly	Ala	Glu	Ala	Asn	Glu	Ala	Ala	
			105					110					115			

ttc	aag	att	gca	cgc	ttg	act	ggc	cgt	tcc	cgc	att	ctg	gct	gca	gtt	499
Phe	Lys	Ile	Ala	Arg	Leu	Thr	Gly	Arg	Ser	Arg	Ile	Leu	Ala	Ala	Val	
		120					125					130				

cat	ggc	ttc	cac	ggc	cgc	acc	atg	ggc	tcc	ctc	gcg	ctg	act	ggc	cag	547
His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu	Ala	Leu	Thr	Gly	Gln	
	135					140				145						

cca	gac	aag	cgt	gaa	gcg	ttc	ctg	cca	atg	cca	agc	ggc	gtg	gag	ttc	595
Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro	Ser	Gly	Val	Glu	Phe	
	150				155					160				165		

tac	cot	tac	ggc	gac	acc	gat	tac	ttg	cgc	aaa	atg	gta	gaa	acc	aac	643
Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	Met	Val	Glu	Thr	Asn	
			170						175					180		

cca	acg	gat	gtg	gct	gct	atc	ttc	ctc	gag	cca	atc	cag	ggc	gaa	acg	691
Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	Ile	Gln	Gly	Glu	Thr	
			185					190					195			

ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739
Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	Ala	Val	Arg	Glu	Leu	
		200					205					210				

09746660-133000

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787  
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly  
 215 220 225  
  
 gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835  
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val  
 230 235 240 245  
  
 ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883  
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile  
 250 255 260  
  
 ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931  
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly  
 265 270 275  
  
 aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979  
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala  
 280 285 290  
  
 aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027  
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala  
 295 300 305  
  
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325  
  
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340  
  
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355  
  
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370  
  
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375 380 385  
  
 atc gca taaaggactc aaacttatga ctt 1296  
 Ile Ala  
 390

&lt;210&gt; 58

&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 58

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly  
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20 25 30

0974660-122200

Asp	Gln	Gly	Asn	Val	Tyr	Ile	Asp	Leu	Leu	Ala	Gly	Ile	Ala	Val	Asn
		35					40					45			
Ala	Leu	Gly	His	Ala	His	Pro	Ala	Ile	Ile	Glu	Ala	Val	Thr	Asn	Gln
	50					55					60				
Ile	Gly	Gln	Leu	Gly	His	Val	Ser	Asn	Leu	Phe	Ala	Ser	Arg	Pro	Val
65					70					75					80
Val	Glu	Val	Ala	Glu	Glu	Leu	Ile	Lys	Arg	Phe	Ser	Leu	Asp	Asp	Ala
				85					90					95	
Thr	Leu	Ala	Ala	Gln	Thr	Arg	Val	Phe	Phe	Cys	Asn	Ser	Gly	Ala	Glu
			100					105					110		
Ala	Asn	Glu	Ala	Ala	Phe	Lys	Ile	Ala	Arg	Leu	Thr	Gly	Arg	Ser	Arg
		115					120					125			
Ile	Leu	Ala	Ala	Val	His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu
	130					135					140				
Ala	Leu	Thr	Gly	Gln	Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro
145					150					155					160
Ser	Gly	Val	Glu	Phe	Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys
				165					170					175	
Met	Val	Glu	Thr	Asn	Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro
			180					185					190		
Ile	Gln	Gly	Glu	Thr	Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys
		195					200					205			
Ala	Val	Arg	Glu	Leu	Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp
	210					215					220				
Glu	Val	Gln	Thr	Gly	Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln
225					230					235					240
His	Asp	Gly	Val	Val	Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly
				245					250					255	
Gly	Gly	Leu	Pro	Ile	Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu
			260					265					270		
Leu	Met	Thr	Pro	Gly	Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val
		275					280					285			
Ala	Cys	Ala	Ala	Ala	Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe
	290					295					300				
Cys	Ala	Glu	Val	Ala	Arg	Lys	Gly	Glu	Leu	Phe	Lys	Glu	Leu	Leu	Ala
305					310					315					320
Lys	Val	Asp	Gly	Val	Val	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly
				325					330					335	
Val	Val	Leu	Glu	Arg	Asp	Val	Ala	Lys	Gln	Ala	Val	Leu	Asp	Gly	Phe
			340					345					350		

[illegible]



Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu  
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Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys  
370 375 380

Ala Ile Ala Glu Thr Ile Ala  
385 390

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<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXC00733

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Met Ser Asn Thr Ala  
1 5

ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag 163  
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys  
10 15 20

gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc 211  
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly  
25 30 35

cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc 259  
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser  
40 45 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307  
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn  
55 60 65

gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca 355  
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser  
70 75 80 85

aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag 403  
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln  
90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca gcc tca gcc att gat 451  
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp  
105 110 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499  
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu  
120 125 130

atc ggt agc ctg ttg tcg ttg ttc cag gcg cgg atg ctc aac cgc atc 547  
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile

09746660 "122200"

135 140 145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595  
 Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile  
 150 155 160 165

cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg 643  
 His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu  
 170 175 180

ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa 691  
 Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln  
 185 190 195

caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg 739  
 Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val  
 200 205 210

ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg 787  
 Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu  
 215 220 225

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835  
 Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg  
 230 235 240 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883  
 Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn  
 250 255 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931  
 Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe  
 265 270 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979  
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 Cys Val  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu  
 20 25 30

Phe Gly Ile Leu Gly His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe  
 35 40 45 \

Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu  
 50 55 60

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Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met  
 65 70 75 80  
 Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala  
 85 90 95  
 Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro  
 100 105 110  
 Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val  
 115 120 125  
 Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg  
 130 135 140  
 Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu  
 145 150 155 160  
 Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile  
 165 170 175  
 Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile  
 180 185 190  
 Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu  
 195 200 205  
 Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu  
 210 215 220  
 Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val  
 225 230 235 240  
 Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln  
 245 250 255  
 Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala  
 260 265 270  
 Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu  
 275 280 285  
 Glu Glu Asn Gln Ala Cys Val  
 290 295

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 <213> Corynebacterium glutamicum

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 <223> RXC00861

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002221 "09991260

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc 96  
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile  
                   20                                  25                                  30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144  
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro  
                   35                                  40                                  45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192  
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile  
                   50                                  55                                  60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240  
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly  
                   65                                  70                                  75                                  80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288  
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro  
                                   85                                  90                                  95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336  
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn  
                                   100                                  105                                  110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384  
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu  
                   115                                  120                                  125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426  
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                   20                                  25                                  30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro  
                   35                                  40                                  45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile  
                   50                                  55                                  60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly  
                   65                                  70                                  75                                  80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro  
                                   85                                  90                                  95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn  
                   100                                  105                                  110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu

09746660 "133300

115 120 125  
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<210> 63  
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Met Asn Asp Ser Arg  
1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163  
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly  
10 15 20

cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211  
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser  
25 30 35

tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259  
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg  
40 45 50

gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307  
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln  
55 60 65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355  
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn  
70 75 80 85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403  
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly  
90 95 100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451  
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln  
105 110 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499  
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys  
120 125 130

tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag 547  
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys  
135 140 145

gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595  
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender	
Male	50.0
Female	50.0
Marital status	
Married	50.0
Single	50.0
Divorced	50.0
Widowed	50.0
Education level	
High school or less	50.0
College or more	50.0
Occupation	
Retired	50.0
Unemployed	50.0
Employed	50.0
Income (USD/month)	
< 1000	50.0
1000-2000	50.0
> 2000	50.0
Health status	
Good	50.0
Fair	50.0
Poor	50.0
Comorbidities	
Hypertension	50.0
Diabetes	50.0
Cholesterol	50.0
Smoking status	
Smoker	50.0
Non-smoker	50.0
Alcohol consumption	
Drinker	50.0
Non-drinker	50.0
Medication use	
Yes	50.0
No	50.0
Medication type	
Antidepressant	50.0
Antipsychotic	50.0
Mood stabilizer	50.0
Other	50.0
Duration of illness (years)	10.0 ± 2.0
Family history of mental illness	
Yes	50.0
No	50.0
Previous hospitalization	
Yes	50.0
No	50.0
Current symptoms	
Depression	50.0
Anxiety	50.0
Mania	50.0
Bipolar disorder	50.0
Schizophrenia	50.0
Other	50.0
Current treatment	
Medication	50.0
Psychotherapy	50.0
Both	50.0
None	50.0
Duration of current treatment (months)	12.0 ± 3.0
Response to treatment	
Yes	50.0
No	50.0
Reason for non-response	
Medication resistance	50.0
Psychotherapy resistance	50.0
Both	50.0
Other	50.0
Current quality of life	
Good	50.0
Fair	50.0
Poor	50.0
Current social support	
Yes	50.0
No	50.0
Current social support type	
Family	50.0
Friends	50.0
Both	50.0
None	50.0
Current social support satisfaction	
Satisfied	50.0
Dissatisfied	50.0
Reason for dissatisfaction	
Lack of support	50.0
Quality of support	50.0
Both	50.0
Other	50.0
Current social support duration (years)	10.0 ± 2.0
Current social support frequency (times/week)	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
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Current social support satisfaction score	1.0 ± 0.5
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Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social support satisfaction score	1.0 ± 0.5
Current social support type score	1.0 ± 0.5
Current social support duration score	1.0 ± 0.5
Current social support frequency score	1.0 ± 0.5
Current social	

150 155 160 165

atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc 643  
 Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile  
 170 175 180

gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac 691  
 Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp  
 185 190 195

ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc 739  
 Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val  
 200 205 210

gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att 787  
 Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile  
 215 220 225

ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt 835  
 Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg  
 230 235 240 245

ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt 883  
 Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg  
 250 255 260

cag aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg 931  
 Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro  
 265 270 275

ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt 979  
 Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu  
 280 285 290

ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac 1027  
 Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp  
 295 300 305

atc aag ctg gat cag act cct cct gat gga cgc cca act 1066  
 Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr  
 310 315 320

<210> 64

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Asn Asp Ser Arg Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly  
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Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln  
 20 25 30

Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala  
 35 40 45

Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp  
 50 55 60

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Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly  
 65 70 75 80  
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly  
 85 90 95  
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly  
 100 105 110  
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg  
 115 120 125  
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu  
 130 135 140  
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu  
 145 150 155 160  
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn  
 165 170 175  
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly  
 180 185 190  
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp  
 195 200 205  
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp  
 210 215 220  
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro  
 225 230 235 240  
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys  
 245 250 255  
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn  
 260 265 270  
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser  
 275 280 285  
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val  
 290 295 300  
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg  
 305 310 315 320  
 Pro Thr

<210> 65  
 <211> 1527  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1504)  
 <223> RXC02095

002221 09994260







455

460

465

tgatgagcag atcgaacacg cag

1527

&lt;210&gt; 66

&lt;211&gt; 468

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 66

Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala  
 1 5 10 15

Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln  
 20 25 30

Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr  
 35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile  
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg  
 65 70 75 80

Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile  
 85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr  
 100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys  
 115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile  
 130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val  
 145 150 155 160

Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys  
 165 170 175

Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr  
 180 185 190

Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr  
 195 200 205

Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala  
 210 215 220

Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val  
 225 230 235 240

Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu  
 245 250 255

Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr  
 260 265 270

004660 16200

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val  
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr  
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala  
 305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu  
 325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg  
 340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu  
 355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu  
 370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser  
 385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp  
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp  
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp  
 435 440 445

Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly  
 450 455 460

Phe Gly Cys Gln  
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<210> 67  
 <211> 295  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXC03185

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tcactgagct gtccgaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113  
 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn  
 1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161  
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe  
 15 20 25

09746660-12200

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209  
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile  
                   30                                  35                                  40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257  
 Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala  
                   45                                  50                                  55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295  
 Ser Arg Glu Ser Leu  
                   60

<210> 68  
 <211> 63  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 68  
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Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys  
                   20                                  25                                  30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr  
                   35                                  40                                  45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu  
           50                                  55                                  60

<210> 69  
 <211> 1170  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1147)  
 <223> RXA00115

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cgtatattgt gacctacacc ccatactggt aggagttttc atg ctc gac aat agt 115  
   Met Leu Asp Asn Ser  
   1                                  5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163  
 Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly  
                   10                                  15                                  20

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct 211  
 Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala  
                   25                                  30                                  35

tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc 259  
 Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu  
                   40                                  45                                  50

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att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac 307  
 Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr  
 55 60 65

atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc 355  
 Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser  
 70 75 80 85

atc aac caa atc ggt aat ggt ttg tgc gtc tcc cct gcc aac acg gct 403  
 Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala  
 90 95 100

gat gac agc atc tgc atg tcc aag ttc ccg aat gtt cgc att ggt gat 451  
 Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp  
 105 110 115

gat gtc gtt gcc cag gac cgg ctg ttg cgc caa gag ttt ggt att acc 499  
 Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr  
 120 125 130

gag ctg ttt gcc gtc gtt ggt ggt tgc atg ggt gcg cag caa acc tat 547  
 Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr  
 135 140 145

gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc 595  
 Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile  
 150 155 160 165

gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act 643  
 Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr  
 170 175 180

ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac 691  
 Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr  
 185 190 195

tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tgc cat ctt 739  
 Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu  
 200 205 210

tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg 787  
 Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp  
 215 220 225

cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctg gcg gac ttc ctg 835  
 Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu  
 230 235 240 245

gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctg aac aac gct 883  
 Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala  
 250 255 260

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931  
 Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu  
 265 270 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979  
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile  
 280 285 290

094660-12200

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027  
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala  
 295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075  
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His  
 310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa 1123  
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys  
 330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct 1170  
 Asn Leu Lys Glu Leu Phe Glu Ser  
 345

<210> 70

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu  
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Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu  
 20 25 30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys  
 35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr  
 50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys  
 65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser  
 85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn  
 100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln  
 115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly  
 130 135 140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His  
 145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe  
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe  
 180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg  
 195 200 205

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cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307  
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu  
 55 60 65

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ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355  
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys  
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403  
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met  
 90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451  
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile  
 105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499  
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile  
 120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547  
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr  
 135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595  
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val  
 150 155 160 165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643  
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser  
 170 175 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691  
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn  
 185 190 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
 215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883  
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

00745660-122000



acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
 360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag 1254  
 Glu Phe Tyr Ile  
 375

<210> 72  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 72  
 Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
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Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His

09746660-122200

180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile  
370 375

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<211> 1210  
<212> DNA  
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<221> CDS  
<222> (101)..(1210)  
<223> FRXA00403

<400> 73  
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Met Pro Thr Leu Ala  
1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211

002221 0999460

Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly  
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259  
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu  
40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307  
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu  
55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355  
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys  
70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403  
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met  
90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451  
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile  
105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499  
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile  
120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547  
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr  
135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595  
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val  
150 155 160 165

ctt gca gtt tot gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643  
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser  
170 175 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691  
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn  
185 190 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883  
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr

00227" 09994250



145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
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Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
340 345 350

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Pro Ser  
370

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Leu His Ser Thr Thr  
1 5

002227 09934760

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163  
Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr  
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aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211  
Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile  
25 30 35  
  
gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259  
Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu  
40 45 50  
  
aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307  
Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys  
55 60 65  
  
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Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr  
70 75 80 85  
  
cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403  
Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met  
90 95 100  
  
aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451  
Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu  
105 110 115  
  
gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499  
Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu  
120 125 130  
  
tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547  
Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr  
135 140 145  
  
cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595  
His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val  
150 155 160 165  
  
cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643  
Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val  
170 175 180  
  
gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687  
Glu Gln Ala Leu Asn Asn Leu  
185

&lt;210&gt; 76

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 76

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly  
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Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe  
20 25 30

09746660-12200

Met	Gln	Gly	Gly	Ile	Gly	Pro	Ile	Pro	Ser	Val	Phe	Asp	Ala	Tyr	Leu
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Thr	Ala	Arg	Gly	Leu	Lys	Thr	Leu	Ala	Val	Arg	Met	Asp	Arg	His	Cys
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Asp	Asn	Ala	Glu	Lys	Ile	Ala	Glu	Phe	Leu	Asp	Ser	Arg	Pro	Glu	Val
65					70					75					80
Ser	Thr	Val	Leu	Tyr	Pro	Gly	Leu	Lys	Asn	His	Pro	Gly	His	Glu	Val
				85					90					95	
Ala	Ala	Lys	Gln	Met	Lys	Arg	Phe	Gly	Gly	Met	Ile	Ser	Val	Arg	Phe
			100					105					110		
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		115					120					125			
Ile	Cys	Leu	Ala	Glu	Ser	Leu	Gly	Gly	Val	Glu	Ser	Leu	Leu	Glu	His
130						135					140				
Pro	Ala	Thr	Met	Thr	His	Gln	Ser	Ala	Ala	Gly	Ser	Gln	Leu	Glu	Val
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Pro	Arg	Asp	Leu	Val	Arg	Ile	Ser	Ile	Gly	Ile	Glu	Asp	Ile	Glu	Asp
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Gln	Pro	Leu	Lys	Leu	Gly	Ala	His	Ala	Val	Leu	His	Ser	Thr	Thr	Lys		
1				5					10					15			
tac	atc	gga	gga	cac	tcc	gac	gtt	gtt	ggc	ggc	ctt	gtg	gtt	acc	aac	96	
Tyr	Ile	Gly	Gly	His	Ser	Asp	Val	Val	Gly	Gly	Leu	Val	Val	Thr	Asn		
			20					25					30				
gac	cag	gaa	atg	gac	gaa	gaa	ctg	ctg	ttc	atg	cag	ggc	ggc	atc	gga	144	
Asp	Gln	Glu	Met	Asp	Glu	Glu	Leu	Leu	Phe	Met	Gln	Gly	Gly	Ile	Gly		
		35					40					45					
ccg	atc	cca	tca	gtt	ttc	gat	gca	tac	ctg	acc	gcc	cgt	ggc	ctc	aag	192	
Pro	Ile	Pro	Ser	Val	Phe	Asp	Ala	Tyr	Leu	Thr	Ala	Arg	Gly	Leu	Lys		
	50					55					60						
acc	ctt	gca	gtg	cgc	atg	gat	cgc	cac	tgc	gac	aac	gca	gaa	aag	atc	240	
Thr	Leu	Ala	Val	Arg	Met	Asp	Arg	His	Cys	Asp	Asn	Ala	Glu	Lys	Ile		

65 70 75 80

gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288  
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
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ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag 336  
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
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 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala  
                     115                    120                    125

gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432  
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser  
                     130                    135                    140

ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480  
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                     145                    150                    155                    160

cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc 528  
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg  
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atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag 576  
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu  
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cag gcc ctc aat aac ctt tagaaactat ttggcgggcaa gca 617  
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Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn  
                     20                    25                    30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly  
                     35                    40                    45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys  
                     50                    55                    60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile  
   65                    70                    75                    80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
                     85                    90                    95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
                     100                    105                    110

0974660-12200



Gln Ala Leu Asn Asn Leu  
195

gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg 403  
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val  
90 95 100

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Divorced	0%
Widowed	0%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
Professional	15.2%
Managerial	12.5%
Technical	18.7%
Service	25.3%
Unemployed	28.3%
Income (USD/month)	
< 1000	12.5%
1000-2000	35.2%
2000-3000	28.7%
> 3000	23.6%
Health insurance	
Yes	85.2%
No	14.8%
Smoking status	
Smoker	18.5%
Non-smoker	81.5%
Alcohol consumption	
Regular	5.2%
Occasional	12.5%
Never	82.3%
Comorbidities	
Hypertension	35.2%
Diabetes	12.5%
Cholesterol	28.7%
Heart disease	15.2%
Stroke	8.5%
Arthritis	22.3%
Depression	10.5%
Other	5.2%



Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser  
260 265 270

[illegible]

Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser  
 275 280 285

Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala  
 290 295 300

Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro  
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Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu  
 325 330 335

Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly  
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 Leu Ser Phe Asp Pro  
 1 5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163  
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro  
 10 15 20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211  
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr  
 25 30 35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259  
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr  
 40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307  
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala  
 55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355  
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala  
 70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403  
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val  
 90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451  
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val  
 105 110 115

0974660-12200







Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender				
Male	52.1			
Female	47.9			
Marital Status				
Married	68.3			
Single	31.7			
Education				
High School	15.2			
Bachelor's	45.8			
Master's	38.9			
PhD	0.1			
Income				
\$10,000-\$20,000	12.5			
\$20,000-\$30,000	28.7			
\$30,000-\$40,000	35.4			
\$40,000-\$50,000	23.1			
\$50,000+	1.3			
Health Status				
Excellent	5.2			
Good	32.1			
Fair	41.3			
Poor	21.4			
Exercise Frequency				
Daily	18.7			
Weekly	35.2			
Monthly	22.5			
Never	23.6			
Stress Level				
Low	10.1			
Medium	38.9			
High	51.0			
Sleep Quality				
Good	65.3			
Fair	28.7			
Poor	5.8			
Dietary Habits				
Healthy	42.1			
Unhealthy	57.9			
Alcohol Consumption				
Regular	15.4			
Occasional	32.1			
Never	52.5			
Tobacco Use				
Regular	8.2			
Occasional	12.3			
Never	79.5			

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                                         Leu Gly Ala Tyr Gly
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tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
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cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
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Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met

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40

45

50

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Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro	
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agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat	355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp	
70 75 80 85	
gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa	403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln	
90 95 100	
gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc	451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly	
105 110 115	
cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg	499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala	
120 125 130	
ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt	547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe	
135 140 145	
cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt	595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu	
150 155 160 165	
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Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala	
170 175 180	
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Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser	
185 190 195	
att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg	739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp	
200 205 210	
gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat	787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp	
215 220 225	
caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc	835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr	
230 235 240 245	
agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta	883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val	
250 255 260	
gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc	931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg	
265 270 275	
ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt	979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val	
280 285 290	

0944660 1 23200

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 295 300 305

gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag 1075  
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys  
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<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

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 35 40 45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val  
 50 55 60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu  
 65 70 75 80

Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp  
 85 90 95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile  
 100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg  
 115 120 125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys  
 130 135 140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro  
 145 150 155 160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe  
 165 170 175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln  
 180 185 190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly  
 195 200 205

Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val  
 210 215 220

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Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe  
 225 230 235 240

Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr  
 245 250 255

Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala  
 260 265 270

Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr  
 275 280 285

Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly  
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Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser  
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Glu Met Leu Ser Lys Asp Ser Cys Asp Leu  
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 <223> RXA02197

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ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac 96  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45

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 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctg acc gaa gca ttg gcc 240  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

gag tac tgg cac tcc cga gtg cgc agc gaa ctg aag ctg aac gac ggt 288  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110

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 130 135 140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528  
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Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
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Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
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Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
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Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140

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 Met Ser Thr Ser Val  
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act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
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ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
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caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259  
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly  
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tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307  
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
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 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
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ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403  
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg  
 90 95 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451  
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala  
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gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt 499  
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly  
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tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat 547  
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr  
 135 140 145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac 595  
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp  
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gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat 691

002222 "09994460

Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp  
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 Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr  
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 ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag 835  
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 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu  
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 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg  
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 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly  
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Pro Ile Met Ile Asp Ser Thr Glu	Pro Glu Val Ile Arg Thr Gly Leu		
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gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac			1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp			
455	460	465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag			1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys			
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cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag			1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln			
490	495	500	
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Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp			
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gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac			1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp			
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tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat			1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp			
535	540	545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca			1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro			
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gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac			1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn			
570	575	580	
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att			1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile			
585	590	595	
gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg			1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro			
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Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln			
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ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa			2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu			
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Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile			
665	670	675	

002221 09994750

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gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg 2227  
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
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aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc 2275  
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
 710 715 720 725

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 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
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ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag 2371  
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
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ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat 2419  
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467  
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
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gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515  
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 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg 2563  
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 Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
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002221-0099460



80

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Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
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 435 440 445  
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 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
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 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
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 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
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 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
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 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
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 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
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 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
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0044560-12200

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Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly  
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Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys  
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser  
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Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser  
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caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259  
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly  
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Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
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His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
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09746660-122200

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tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451  
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala  
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gat gag atg ggg ccg ggc cga aac ggc atg ccg cgt ttc gtg gtt ggt 499  
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly  
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tcc ctg gga cct gga acg aag ctt cca tcc ctg ggc cat gca ccg tat 547  
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 135 140 145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac 595  
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp  
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ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag 835  
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atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg 883  
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tcc gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca 931  
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 Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe  
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cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag 1075  
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 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc 1267  
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt 1315  
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 390 395 400 405

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 455 460 465

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gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac 1651  
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
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gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac 1699  
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
 520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat 1747  
 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
 535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca 1795  
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
 550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac 1843

004424-0999460

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Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe	Leu	Asn	Glu	Cys	Ile		
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gag	gct	ggc	ctg	gac	tct	gcg	att	gcg	cac	agc	tcc	aag	att	ttg	ccg	1939	
Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser	Ser	Lys	Ile	Leu	Pro		
		600					605					610					
atg	aac	cgc	att	gat	gat	cgc	cag	cgc	gaa	gtg	gcg	ttg	gat	atg	gtc	1987	
Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Glu	Val	Ala	Leu	Asp	Met	Val		
	615					620					625						
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Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu	Gln	Glu	Phe	Met	Gln		
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ctg	ttt	gag	ggc	gtt	tct	gct	gcc	gat	gcc	aag	gat	gct	cgc	gct	gaa	2083	
Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys	Asp	Ala	Arg	Ala	Glu		
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cag	ctg	gcc	gct	atg	cct	ttg	ttt	gag	cgt	ttg	gca	cag	cgc	atc	atc	2131	
Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu	Ala	Gln	Arg	Ile	Ile		
			665					670					675				
gac	ggc	gat	aag	aat	ggc	ctt	gag	gat	gat	ctg	gaa	gca	ggc	atg	aag	2179	
Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu	Glu	Ala	Gly	Met	Lys		
		680					685					690					
gag	aag	tct	cct	att	gcg	atc	atc	aac	gag	gac	ctt	ctc	aac	ggc	atg	2227	
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Geographical location	
Country	Spain
Region	Madrid
City	Madrid
Address	Avda. de la Constitución, 100
Postal code	28002
Phone	+34 91 540 00 00
Fax	+34 91 540 00 01
E-mail	info@ciencia.es
Website	www.ciencia.es
Contact person	
Name	Dr. Juan Carlos Rodríguez Cordero
Position	Director General de Investigación Científica
Address	Avda. de la Constitución, 100
Postal code	28002
Phone	+34 91 540 00 00
Fax	+34 91 540 00 01
E-mail	info@ciencia.es
Website	www.ciencia.es
Financial information	
Year of establishment	1980
Year of last financial statement	2000
Turnover	100 000 000
Number of employees	100
Number of research projects	100
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1. General Information	
1.1. Name of the Project	1.2. Date of Submission
1.3. Name of the Applicant	1.4. Address of the Applicant
1.5. Contact Person	1.6. Telephone Number
1.7. E-mail Address	1.8. Fax Number
1.9. Website	1.10. Other Information
2. Project Description	
2.1. Objectives of the Project	2.2. Justification of the Project
2.3. Methodology	2.4. Expected Results
2.5. Budget	2.6. Timeline
2.7. Risk Assessment	2.8. Conclusion
3. References	
3.1. List of References	3.2. Other References
3.3. Bibliography	3.4. Appendix
3.5. Declaration	3.6. Signature
3.7. Stamp	3.8. Date
3.9. Other Information	3.10. Final Remarks
4. Evaluation	
4.1. Evaluation Criteria	4.2. Evaluation Results
4.3. Evaluation Comments	4.4. Evaluation Date
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 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc 1315  
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 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363  
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
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gaa gga cag tac gag aac gag gtc tac cgt ctg 1396  
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&lt;210&gt; 102

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 102

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Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
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				Met	Thr	Ser	Asn	Phe								
				1				5								
tct	tcc	act	gtc	gct	ggg	ctt	cct	cgc	atc	gga	gcg	aag	cgt	gaa	ctg	163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu	
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aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggg	cgc	gaa	211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	
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Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu	
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Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala	
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Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp	
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gac	atc	gct	gat	cat	gaa	aac	gat	ggg	ctc	cca	ctg	tgg	att	gac	cgc	403
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg	
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Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met	
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Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser	
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gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547
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ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctg atc aag 691  
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
 185 190 195

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 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
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094660-1320

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 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
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 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
 680 685 690  
  
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 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
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 Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
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 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
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 <213> Corynebacterium glutamicum  
  
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 Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
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 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 50 55 60  
  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80  
  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95  
  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
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 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125

004460 "122" 0994460



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 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
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 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 180 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
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 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
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09746660-122300



<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

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Met Thr Ser Asn Phe  
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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu  
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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu  
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tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307  
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala  
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gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403  
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135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595  
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150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643  
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0974660-42230



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&lt;210&gt; 106

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

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Pro	Ala	Gln 115	Ala	Met	Thr	Lys	Trp 120	Phe	Asp	Thr	Asn	Tyr 125	His	Tyr	Leu	
Val	Pro 130	Glu	Leu	Ser	Ala	Asp 135	Thr	Arg	Phe	Val	Leu 140	Asp	Ala	Ser	Ala	
Leu 145	Ile	Glu	Asp	Leu	Arg 150	Cys	Gln	Gln	Val	Arg 155	Gly	Val	Asn	Ala	Arg 160	
Pro	Val	Leu	Val	Gly 165	Pro	Leu	Thr	Phe	Leu 170	Ser	Leu	Ala	Arg	Thr 175	Thr	
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Tyr	Phe	Gly	Ser	Gly 245	Asp	Gln	Ala	Leu	Asn 250	Thr	Leu	Ala	Gly	Ile 255	Gly	
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Ala	Ala	Trp 275	Lys	Gly	Glu	Glu	Leu 280	Leu	Val	Ala	Gly	Ile 285	Val	Asp	Gly	
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Arg 305	Leu	Ala	Ala	Arg	Gly 310	Pro	Ile	Ala	Val	Ser 315	Thr	Ser	Cys	Ser	Leu 320	
Leu	His	Val	Pro	Tyr 325	Thr	Leu	Glu	Ala	Glu 330	Asn	Ile	Glu	Pro	Glu 335	Val	
Arg	Asp	Trp	Leu 340	Ala	Phe	Gly	Ser	Glu 345	Lys	Ile	Thr	Glu	Val 350	Lys	Leu	
Leu	Ala	Asp 355	Ala	Leu	Ala	Gly	Asn 360	Ile	Asp	Ala	Ala	Ala 365	Phe	Asp	Ala	
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Gly	Glu	Glu 35	Glu	Phe	Phe	Gln	Ile 40	Leu	Gln	Ser	Ser	Val 45	Asp	Asp	Val
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Tyr 65	Gly	His	Val	Thr	Ser 70	Gly	Ala	Val	Asp	Phe 75	Gly	Ala	Trp	Trp	Asn 80
Tyr	Ser	Phe	Thr	Arg 85	Leu	Gly	Gly	Leu	Thr 90	Met	Thr	Asp	Thr	Asp 95	Arg
Trp	Ala	Ser	Gln 100	Glu	Ala	Val	Arg	Ser 105	Thr	Pro	Gly	Asn	Ile 110	Glu	Leu
Thr	Ser	Phe 115	Ser	Asp	Arg	Arg	Asp 120	Arg	Ala	Leu	Phe	Ser 125	Glu	Ala	Tyr
Glu 130	Asp	Pro	Val	Ser	Gly	Ile 135	Phe	Thr	Gly	Arg	Ala 140	Ser	Val	Gly	Asn
Pro 145	Glu	Phe	Thr	Gly	Pro 150	Ile	Thr	Tyr	Ile	Gly 155	Gln	Glu	Glu	Thr	Gln 160
Thr	Asp	Val	Asp	Leu 165	Leu	Lys	Lys	Gly	Met 170	Asn	Ala	Ala	Gly	Ala 175	Thr
Asp	Gly	Phe	Val 180	Ala	Ala	Leu	Ser	Pro 185	Gly	Ser	Ala	Ala	Arg 190	Leu	Thr
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Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
 305 310 315 320

Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
 370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400

Phe

<210> 111  
 <211> 548  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(525)  
 <223> FRXA02648

<400> 111

gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca	48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro	
1 5 10 15	
agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc	96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile	
20 25 30	
aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc	144

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
           35                          40                          45  
 tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192  
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
           50                          55                          60  
 gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240  
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
           65                          70                          75                          80  
 gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288  
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
                           85                          90                          95  
 aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336  
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
                           100                          105                          110  
 tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384  
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
                           115                          120                          125  
 cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432  
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
                           130                          135                          140  
 tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
           145                          150                          155                          160  
 gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
                           165                          170                          175  
 taagctagac aacgagggtt gct 548

&lt;210&gt; 112

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 112

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro  
           1                          5                          10                          15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
                           20                          25                          30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
           35                          40                          45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
           50                          55                          60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
           65                          70                          75                          80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
                           85                          90                          95

03231 03937450



cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145

oct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

<210> 114

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn

0924660-1336





408

<400> 116

<400> 117

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
55 60 65

[illegible]

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499  
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr  
 120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547  
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu  
 135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595  
 Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu  
 150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643  
 Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe  
 170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat 691  
 Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn  
 185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739  
 Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly  
 200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787  
 Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp  
 215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835  
 Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu  
 230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883  
 Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val  
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931  
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala  
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979  
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp  
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg 1027  
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu  
 295 300 305

002227-00994260

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg 1075  
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val  
 310 315 320 325  
 agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg 1123  
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala  
 330 335 340  
 att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355  
 gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370  
 ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385  
 ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405  
 tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420  
 cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435  
 ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450  
 gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507  
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465  
 gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555  
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485  
 gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500  
 cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515  
 ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530  
 gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747  
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
 535 540 545  
 att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795

002227" 09997260

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
 550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc  
 Val Ala Tyr

1827

&lt;210&gt; 118

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 118

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
 1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
 20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
 35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
 50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
 65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
 85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
 115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
 130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
 145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
 165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe  
 245 250 255

05746560-122000

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro  
 530 535 540  
 Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr  
 545 550 555 560  
 Arg Ala Ala Pro Val Val Ala Tyr  
 565

002227-0899460-122200

ggt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc 643  
Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr  
170 175 180

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 ± 2.0
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	30 (60.0%)
Unemployed	20 (40.0%)
Income (USD/month)	1,200 ± 300
Health status	
Good	30 (60.0%)
Fair	20 (40.0%)
Poor	10 (20.0%)
Comorbidities	
Hypertension	20 (40.0%)
Diabetes	10 (20.0%)
Cholesterol	15 (30.0%)
Arthritis	10 (20.0%)
Depression	5 (10.0%)
Other	5 (10.0%)
Medication use	
Yes	30 (60.0%)
No	20 (40.0%)
Medication type	
Antidepressants	10 (20.0%)
Antipsychotics	5 (10.0%)
Anticholinergics	5 (10.0%)
Other	10 (20.0%)
Adherence	
High	20 (40.0%)
Low	10 (20.0%)
Very low	5 (10.0%)
Non-adherent	15 (30.0%)
Reasons for non-adherence	
Lack of knowledge	5 (10.0%)
Lack of motivation	5 (10.0%)
Side effects	5 (10.0%)
Other	5 (10.0%)

cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat 691  
 Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp  
 185 190 195

acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg 739  
 Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp  
 200 205 210

ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac 787  
 Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp  
 215 220 225

gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac 835  
 Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn  
 230 235 240 245

cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg 883  
 Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu  
 250 255 260

acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat 931  
 Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His  
 265 270 275

ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct 979  
 Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser  
 280 285 290

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc 1027  
 Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly  
 295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca 1075  
 Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala  
 310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc 1123  
 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly  
 330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg 1171  
 Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu  
 345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac 1219  
 Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr  
 360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt 1267  
 Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu  
 375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag 1315  
 Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys  
 390 395 400 405

ttg gcc taaaaatctg atgtagtatc ttc 1344  
 Leu Ala

002222 " 09994460

$\langle 400 \rangle$  120

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu  
20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr  
35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser  
50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile  
65 70 75 80

Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val  
85 90 95

Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp  
100 105 110

Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg  
115 120 125

Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu  
130 135 140

Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser  
145 150 155 160

Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg  
165 170 175

Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg  
180 185 190

Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu  
195 200 205

Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp  
210 215 220

Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile  
225 230 235 240

Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met  
245 250 255

Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly  
260 265 270

Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser  
275 280 285

[illegible]



Arg Ala Ala Leu Lys Leu Ala  
405

23

23

18

[illegible]

<210> 124  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 124  
 gtaaaacgac ggccagt

18

<210> 125  
 <211> 4334  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 gacaatcaat gaagctatgt ctgaatttag cgtgtcacgt cagaccgtga atagagcact 120  
 taagtctgcg ggcattgaac ttccacgagg acgcgtaaa gcttcccagt aaatgtgcca 180  
 tctcgtaggc agaaaaacggt tcccccgta ggggtctctc tottggcctc ctttctaggt 240  
 cgggctgatt gctcttgaag ctctctaggg gggctcacac cataggcaga taacggttcc 300  
 ccaccggctc acctcgtaag cgcacaagga ctgctcccaa agatcttcaa agccactgcc 360  
 gcgactccgc ttgcogaagc cttgccccgc ggaaatttcc tccaccgagt tctgacacac 420  
 ccctatgcca agcttcttcc accctaaatt cgagagattg gattcttacc gtggaaattc 480  
 ttgcacaaaa tctgcccctg atcgcccttg cgacgttgct cgcggcgggtg ccgctggttg 540  
 cgcttggtt gaccgaattg atcagcttgc atgcctgcag gtcgacggat ccccggttg 600  
 gaaagccacg ttgtgtctca aaatctctga tgttacattg cacaagataa aaatatatca 660  
 tcatgaacaa taaaactgtc tgcttacata aacagtaata caaggggtgt tatgagccat 720  
 attcaacggg aaacgtcttg ctcgaggccg cgattaaatt ocaacatgga tgctgattta 780  
 tatgggtata aatgggctcg cgataatgtc gggcaatcag gtgcgacaat ctatcgattg 840  
 tatgggaagc ccgatgcgcc agagttgttt ctgaaacatg gcaaaggtag cgttgccaat 900  
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